

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Lin, Lih-Ling  
Graham, James

(ii) TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR  
INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND  
BINDING

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.  
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(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Brown, Scott A.  
(B) REGISTRATION NUMBER: 32,724  
(C) REFERENCE/DOCKET NUMBER: GI5258

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## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1571 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 2..529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G	ATC	CCC	AGG	GTG	GAC	CTC	CGG	GTG	TGG	CAG	GAC	TGC	TGT	GAA	GAC	46
Ile	Pro	Arg	Val	Asp	Leu	Arg	Val	Trp	Gln	Asp	Cys	Cys	Glu	Asp		
1				5					10					15		



GAAACAGGTT TGCTTTCAGC TGCTACTTGC ACACATACTG CCTAGTTGTG AACCAAATGT 1359  
 GAAAAAACCT CCTTCATCCC ATTGTGTATC TGATACCTGC CGAGGGCCAA GGGTGTGTGT 1419  
 TGACAACGCC GCTCCCAGCC GGCCCTGGTT GCGTCCACGT CCTGAACAAG AGCCGCTTCC 1479  
 GGATGGCTCT TCCCAAGGGA GGAGGAGCTC AAGTGTCTGG AACTGTCTAA CTTCAGGTTG 1539  
 TGTGAGTGCG TTAATAAAAAA AAAAAAAAAA AA 1571

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 176 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp Cys  
 1 5 10 15  
 Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly Arg  
 20 25 30  
 Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys Thr  
 35 40 45  
 Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu Ser  
 50 55 60  
 Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr Asn  
 65 70 75 80  
 Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp Leu  
 85 90 95  
 Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu Cys  
 100 105 110  
 Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys Lys  
 115 120 125  
 Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys Phe  
 130 135 140  
 Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile Pro  
 145 150 155 160  
 Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys Pro  
 165 170 175

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1088 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

G AAA AAA GGA GGT AAA ACA GAA CAG GAT GGC TAT CAG AAA CCC ACC	46
Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr	
1 5 10 15	
AAC AAA CAC TTC ACG CAG AGT CCC AAG AAG TCA GTG GCC GAC CTG CTG	94
Asn Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu	
20 25 30	
GGG TCC TTT GAA GGC AAA CGA AGA CTC CTT CTG ATC ACT GCT CCC AAG	142
Gly Ser Phe Glu Gly Lys Arg Arg Leu Leu Leu Ile Thr Ala Pro Lys	
35 40 45	
GCT GAG AAC AAT ATG TAT GTG CAA CAA CGT GAT GAA TAT CTG GAA AGT	190
Ala Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser	
50 55 60	
TTC TGC AAG ATG GCT ACC AGG AAA ATC TCT GTG ATC ACC ATC TTC GGC	238
Phe Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly	
65 70 75	
CCT GTC AAC AAC AGC ACC ATG AAA ATC GAC CAC TTT CAG CTA GAT AAT	286
Pro Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn	
80 85 90 95	
GAG AAG CCC ATG CGA GTG GTG GAT GAT GAA GAC TTG GTA GAC CAG CGT	334
Glu Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg	
100 105 110	
CTC ATC AGC GAG CTG AGG AAA GAG TAC GGA ATG ACC TAC AAT GAC TTC	382
Leu Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe	
115 120 125	
TTC ATG GTG CTA ACA GAT GTG GAT CTG AGA GTC AAG CAA TAC TAT GAG	430
Phe Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu	
130 135 140	
GTA CCA ATA ACA ATG AAG TCT GTG TTT GAT CTG ATC GAT ACT TTC CAG	478
Val Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln	
145 150 155	
TCC CGA ATC AAA GAT ATG GAG AAG CAG AAG AAG GAG GGC ATT GTT TGC	526
Ser Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys	
160 165 170 175	
AAA GAG GAA GTT GGG GGA GTG TTA GAA CTG TTC CCA ATT AAT GGG AGC	574
Lys Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser	
180 185 190	
TCT GTT GTT GAG CGA GAA GAC GTA CCA GCC CAT TTG GTG AAA GAC ATT	622
Ser Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile	
195 200 205	
CGT AAC TAT TTT CAA GTG AGC CCG GAG TAC TTC TCC ATG CTT CTA GTC	670
Arg Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val	
210 215 220	
GGA AAA GAC GGA AAT GTC AAA TCC TGG TAT CCT TCC CCA ATG TGG TCC	718
Gly Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser	
225 230 235	

ATG GTG ATT GTG TAC GAT TTA ATT GAT TCG ATG CAA CTT CGG AGA CAG Met Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln 240 245 250 255	766
GAA ATG GCG ATT CAG CAG TCA CTG GGG ATG CGC TGC CAG AAG ATG AGT Glu Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser 260 265 270	814
ATG CAG GCT ATG GTT ACC ATA GTT ACC ACC AAG GAT ACC AGG ATG GTT Met Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val 275 280 285	862
ACC AGG ATG ACT ACC GTC ATC ATG AGA GTT ATC ACC ATG GAT ACC CTT Thr Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu 290 295 300	910
ACT GAG CAG AAA TAT GTA ACC TTA GAC TCA GCC AGT TTC CTC TGC AGC Thr Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser 305 310 315	958
TGC TAAAACTACA TGTGGCCAGC TCCATTCTTC CACACTGCGT ACTACATTTC Cys 320	1011
CTGCCTTTTT CTTTCAGTGT TTTTCTAAGA CTAAATAAAT AGCAAACTTT CACCTAAAAA	1071
AAAAAAAAAA AAAAAA	1088

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr Asn
1      5      10      15
Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu Gly
20      25      30
Ser Phe Glu Gly Lys Arg Arg Leu Leu Ile Thr Ala Pro Lys Ala
35      40      45
Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser Phe
50      55      60
Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro
65      70      75      80
Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu
85      90      95
Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu
100     105     110
Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe
115     120     125
Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val
130     135     140

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Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser  
 145 150 155 160

Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys  
 165 170 175

Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser  
 180 185 190

Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg  
 195 200 205

Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val Gly  
 210 215 220

Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser Met  
 225 230 235 240

Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln Glu  
 245 250 255

Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser Met  
 260 265 270

Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val Thr  
 275 280 285

Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu Thr  
 290 295 300

Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser Cys  
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1759 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

C AAA AAC TTC TTC CTG ACG AAT CGC GCC AGG GAG CGC TCA GAC ACC	46
Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr	
1 5 10 15	
TTC ATC AAC CTC CGG GAG GTG CTC AAC CGC TTC AAG CTG CCG CCA GGA	94
Phe Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly	
20 25 30	
GAG TAC ATT CTC GTG CCT TCC ACC TTC GAA CCC AAC AAG GAT GGG GAT	142
Glu Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp	
35 40 45	

TTC TGC ATC CGG GTC TTT TCT GAA AAG AAA GCT GAC TAC CAA GCT GTC	190
Phe Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val	
50 55 60	
GAT GAT GAA ATC GAG GCC AAT CTT GAA GAG TTC GAC ATC AGC GAG GAT	238
Asp Asp Glu Ile Glu Ala Asn Leu Glu Glu Phe Asp Ile Ser Glu Asp	
65 70 75	
GAC ATT GAT GAT GGA TTC AGG AGA CTG TTT GCC CAG TTG GCA GGA GAG	286
Asp Ile Asp Asp Gly Phe Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu	
80 85 90 95	
GAT GCG GAG ATC TCT GCC TTT GAG CTG CAG ACC ATC CTG AGA AGG GTT	334
Asp Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val	
100 105 110	
CTA GCA AAG CGC CAA GAT ATC AAG TCA GAT GGC TTC AGC ATC GAG ACA	382
Leu Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr	
115 120 125	
TGC AAA ATT ATG GTT GAC ATG CTA GAT TCG GAC GGG AGT GGC AAG CTG	430
Cys Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu	
130 135 140	
GGG CTG AAG GAG TTC TAC ATT CTC TGG ACG AAG ATT CAA AAA TAC CAA	478
Gly Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln	
145 150 155	
AAA ATT TAC CGA GAA ATC GAC GTT GAC AGG TCT GGT ACC ATG AAT TCC	526
Lys Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser	
160 165 170 175	
TAT GAA ATG CGG AAG GCA TTA GAA GAA GCA GGT TTC AAG ATG CCC TGT	574
Tyr Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys	
180 185 190	
CAA CTC CAC CAA GTC ATC GTT GCT CGG TTT GCA GAT GAC CAG CTC ATC	622
Gln Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile	
195 200 205	
ATC GAT TTT GAT AAT TTT GTT CGG TGT TTG GTT CGG CTG GAA ACG CTA	670
Ile Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu	
210 215 220	
TTC AAG ATA TTT AAG CAG CTG GAT CCC GAG AAT ACT GGA ACA ATA GAG	718
Phe Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu	
225 230 235	
CTC GAC CTT ATC TCT TGG CTC TGT TTC TCA GTA CTT TGAAGTTATA	764
Leu Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu	
240 245 250	
ACTAATCTGC CTGAAGACTT CTCATGATGG AAAATCAGCC AAGGACTAAG CTTCCATAGA	824
AATACACTTT GTATCTGGAC CTCAAAATTA TGGGAACATT TACTTAAACG GATGATCATA	884
GCTGAAAATA ATGATACTGT CAATTTGAGA TAGCAGAAGT TTCACACATC AAAGTAAAAG	944
ATTTGCATAT CATTATACTA AATGCAAATG AGTCGCTTAA CCCTTGACAA GGTCAAAGAA	1004
AGCTTTAAAT CTGTAAATAG TATACACTTT TTACTTTTAC ACACTTTCCT GTTCATAGCA	1064
ATATTAAATC AGGAAAAAAA AATGCAGGGA GGTATTTAAC AGCTGAGCAA AAACATTGAG	1124
TCGCTCTCAA AGGACACGAG GCCCTTGGCA GGAATATTT AAAGCAACTT CAAAGTTTAA	1184
ATGCAGCTGT TGATTCTACC AAACAACAGT CCAAGATTAC CATTTCCCAAT GAGCCAACTG	1244

GGAAACATGG TATATCATGA AGTAATCTTG TCAAGGCATC TGGAGAGTCC AGGAGAGAAG 1304  
 ACTCACCTCT GTCGCTTGGG TTAAACAAGA GACAGGTTTT GTAGAATATT GATTGGTAAT 1364  
 AGTAAATCGT TCTCCTTACA ATCAAGTTCT TGACCCTATT CGGCCTTATA CATCTGGTCT 1424  
 TACAAAGACC AAAGGGATCC TGCCTTGAT CAACTGAACC AGTATGCCAA AACCAGGCAT 1484  
 CCAATTTGTA AACCAATTAT GATAAAGGAC AAAATAAGCT GTTTGCCACC TCAAACTTT 1544  
 ATGAACTTCA CCACCACTAG TGTCTGTCCA TGGAGTTAGA GGGGACATCA CTTAGAAGTT 1604  
 CTTATAGAAA GGACACAAGT TTGTTTCCTG GCTTTACCTT GGGAAAATGC TAGCAACATT 1664  
 ATAGAAATTT TGCCTTGTG CCTTATCTTC TTCAAATGT ACTGTTAAAT AAAAAATAAG 1724  
 GGTTACCCCA TGCAATCAAA AAAAAAAAAA AAAAA 1759

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr Phe  
 1 5 10 15  
 Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly Glu  
 20 25 30  
 Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp Phe  
 35 40 45  
 Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val Asp  
 50 55 60  
 Asp Glu Ile Glu Ala Asn Leu Glu Glu Phe Asp Ile Ser Glu Asp Asp  
 65 70 75 80  
 Ile Asp Asp Gly Phe Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu Asp  
 85 90 95  
 Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val Leu  
 100 105 110  
 Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr Cys  
 115 120 125  
 Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu Gly  
 130 135 140  
 Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln Lys  
 145 150 155 160  
 Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser Tyr  
 165 170 175  
 Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys Gln  
 180 185 190



Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile Ile  
 195 200 205  
 Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu Phe  
 210 215 220  
 Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu Leu  
 225 230 235 240  
 Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu  
 245 250

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 700 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Gly Ile Ala Ala Lys Leu Ala Lys Asp Arg Glu Ala Ala Glu  
 1 5 10 15  
 Gly Leu Gly Ser His Glu Arg Ala Ile Lys Tyr Leu Asn Gln Asp Tyr  
 20 25 30  
 Glu Ala Leu Arg Asn Glu Cys Leu Glu Ala Gly Thr Leu Phe Gln Asp  
 35 40 45  
 Pro Ser Phe Pro Ala Ile Pro Ser Ala Leu Gly Phe Lys Glu Leu Gly  
 50 55 60  
 Pro Tyr Ser Ser Lys Thr Arg Gly Met Arg Trp Lys Arg Pro Thr Glu  
 65 70 75 80  
 Ile Cys Ala Asp Pro Gln Phe Ile Ile Gly Gly Ala Thr Arg Thr Asp  
 85 90 95  
 Ile Cys Gln Gly Ala Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Ala  
 100 105 110  
 Ser Leu Thr Leu Asn Glu Glu Ile Leu Ala Arg Val Val Pro Leu Asn  
 115 120 125  
 Gln Ser Phe Gln Glu Asn Tyr Ala Gly Ile Phe His Phe Gln Phe Trp  
 130 135 140  
 Gln Tyr Gly Glu Trp Val Glu Val Val Val Asp Asp Arg Leu Pro Thr  
 145 150 155 160  
 Lys Asp Gly Glu Leu Leu Phe Val His Ser Ala Glu Gly Ser Glu Phe  
 165 170 175  
 Trp Ser Ala Leu Leu Glu Lys Ala Tyr Ala Lys Ile Asn Gly Cys Tyr  
 180 185 190  
 Glu Ala Leu Ser Gly Gly Ala Thr Thr Glu Gly Phe Glu Asp Phe Thr  
 195 200 205

100-44360

Gly	Gly	Ile	Ala	Glu	Trp	Tyr	Glu	Leu	Lys	Lys	Pro	Pro	Pro	Asn	Leu
210						215					220				
Phe	Lys	Ile	Ile	Gln	Lys	Ala	Leu	Gln	Lys	Gly	Ser	Leu	Leu	Gly	Cys
225					230					235					240
Ser	Ile	Asp	Ile	Thr	Ser	Ala	Ala	Asp	Ser	Glu	Ala	Ile	Thr	Phe	Gln
				245					250					255	
Lys	Leu	Val	Lys	Gly	His	Ala	Tyr	Ser	Val	Thr	Gly	Ala	Glu	Glu	Val
			260					265					270		
Glu	Ser	Asn	Gly	Ser	Leu	Gln	Lys	Leu	Ile	Arg	Ile	Arg	Asn	Pro	Trp
		275					280					285			
Gly	Glu	Val	Glu	Trp	Thr	Gly	Arg	Trp	Asn	Asp	Asn	Cys	Pro	Ser	Trp
	290					295					300				
Asn	Thr	Ile	Asp	Pro	Glu	Glu	Arg	Glu	Arg	Leu	Thr	Arg	Arg	His	Glu
305					310					315					320
Asp	Gly	Glu	Phe	Trp	Met	Ser	Phe	Ser	Asp	Phe	Leu	Arg	His	Tyr	Ser
				325					330					335	
Arg	Leu	Glu	Ile	Cys	Asn	Leu	Thr	Pro	Asp	Thr	Leu	Thr	Ser	Asp	Thr
			340					345					350		
Tyr	Lys	Lys	Trp	Lys	Leu	Thr	Lys	Met	Asp	Gly	Asn	Trp	Arg	Arg	Gly
		355					360					365			
Ser	Thr	Ala	Gly	Gly	Cys	Arg	Asn	Tyr	Pro	Asn	Thr	Phe	Trp	Met	Asn
	370					375					380				
Pro	Gln	Tyr	Leu	Ile	Lys	Leu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Asp
385					390					395					400
Gly	Glu	Ser	Gly	Cys	Thr	Phe	Leu	Val	Gly	Leu	Ile	Gln	Lys	His	Arg
				405					410					415	
Arg	Arg	Gln	Arg	Lys	Met	Gly	Glu	Asp	Met	His	Thr	Ile	Gly	Phe	Gly
			420					425					430		
Ile	Tyr	Glu	Val	Pro	Glu	Glu	Leu	Ser	Gly	Gln	Thr	Asn	Ile	His	Leu
		435					440					445			
Ser	Lys	Asn	Phe	Phe	Leu	Thr	Asn	Arg	Ala	Arg	Glu	Arg	Ser	Asp	Thr
	450					455					460				
Phe	Ile	Asn	Leu	Arg	Glu	Val	Leu	Asn	Arg	Phe	Lys	Leu	Pro	Pro	Gly
465					470					475					480
Glu	Tyr	Ile	Leu	Val	Pro	Ser	Thr	Phe	Glu	Pro	Asn	Lys	Asp	Gly	Asp
				485					490					495	
Phe	Cys	Ile	Arg	Val	Phe	Ser	Glu	Lys	Lys	Ala	Asp	Tyr	Gln	Ala	Val
			500					505					510		
Asp	Asp	Glu	Ile	Glu	Ala	Asn	Leu	Glu	Glu	Phe	Asp	Ile	Ser	Glu	Asp
		515					520					525			
Asp	Ile	Asp	Asp	Gly	Val	Arg	Arg	Leu	Phe	Ala	Gln	Leu	Ala	Gly	Glu
	530					535					540				
Asp	Ala	Glu	Ile	Ser	Ala	Phe	Glu	Leu	Gln	Thr	Ile	Leu	Arg	Arg	Val
545					550					555					560

Leu	Ala	Lys	Arg	Gln	Asp	Ile	Lys	Ser	Asp	Gly	Phe	Ser	Ile	Glu	Thr
				565					570					575	
Cys	Lys	Ile	Met	Val	Asp	Met	Leu	Asp	Ser	Asp	Gly	Ser	Gly	Lys	Leu
			580					585					590		
Gly	Leu	Lys	Glu	Phe	Tyr	Ile	Leu	Trp	Thr	Lys	Ile	Gln	Lys	Tyr	Gln
		595					600					605			
Lys	Ile	Tyr	Arg	Glu	Ile	Asp	Val	Asp	Arg	Ser	Gly	Thr	Met	Asn	Ser
	610					615					620				
Tyr	Glu	Met	Arg	Lys	Ala	Leu	Glu	Glu	Ala	Gly	Phe	Lys	Met	Pro	Cys
625					630					635					640
Gln	Leu	His	Gln	Val	Ile	Val	Ala	Arg	Phe	Ala	Asp	Asp	Gln	Leu	Ile
				645					650					655	
Ile	Asp	Phe	Asp	Asn	Phe	Val	Arg	Cys	Leu	Val	Arg	Leu	Glu	Thr	Leu
			660					665					670		
Phe	Lys	Ile	Phe	Lys	Gln	Leu	Asp	Pro	Glu	Asn	Thr	Gly	Thr	Ile	Glu
		675					680					685			
Leu	Asp	Leu	Ile	Ser	Trp	Leu	Cys	Phe	Ser	Val	Leu				
	690					695					700				

644330